FIG. 1

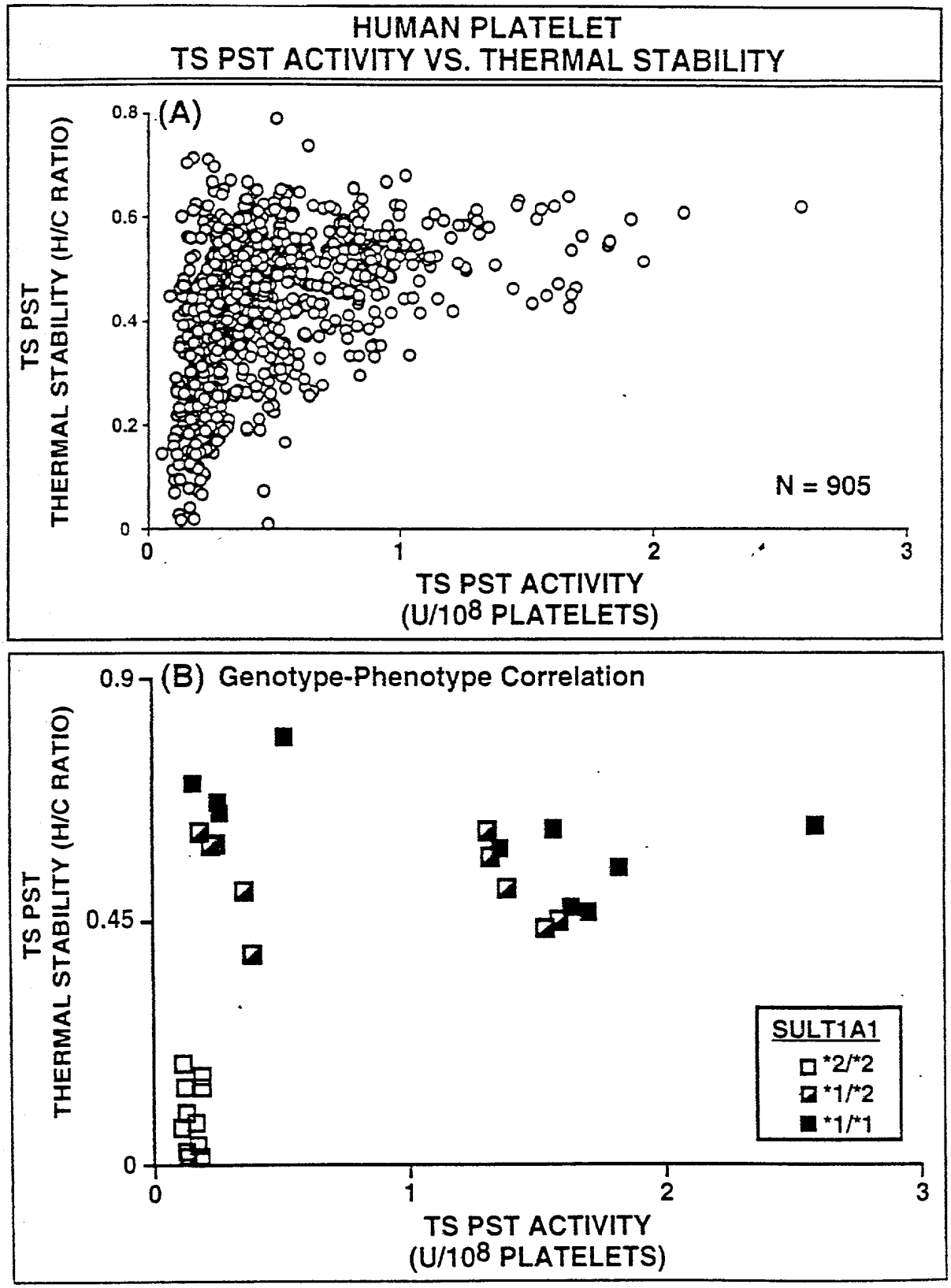

HUMAN PLATELET
TS PST ACTIVITY VS. THERMAL STABILITY
(A)
TS PST
THERMAL STABILITY (H/C RATIO)
0.8
0.6
0.4
0.2
0
N = 905
0
1
2
3
TS PST ACTIVITY
(U/10^8 PLATELETS)
(B) Genotype-Phenotype Correlation
0.9
0.45
0
SULT1A1
*2/*2
*1/*2
*1/*1

FIG. 2

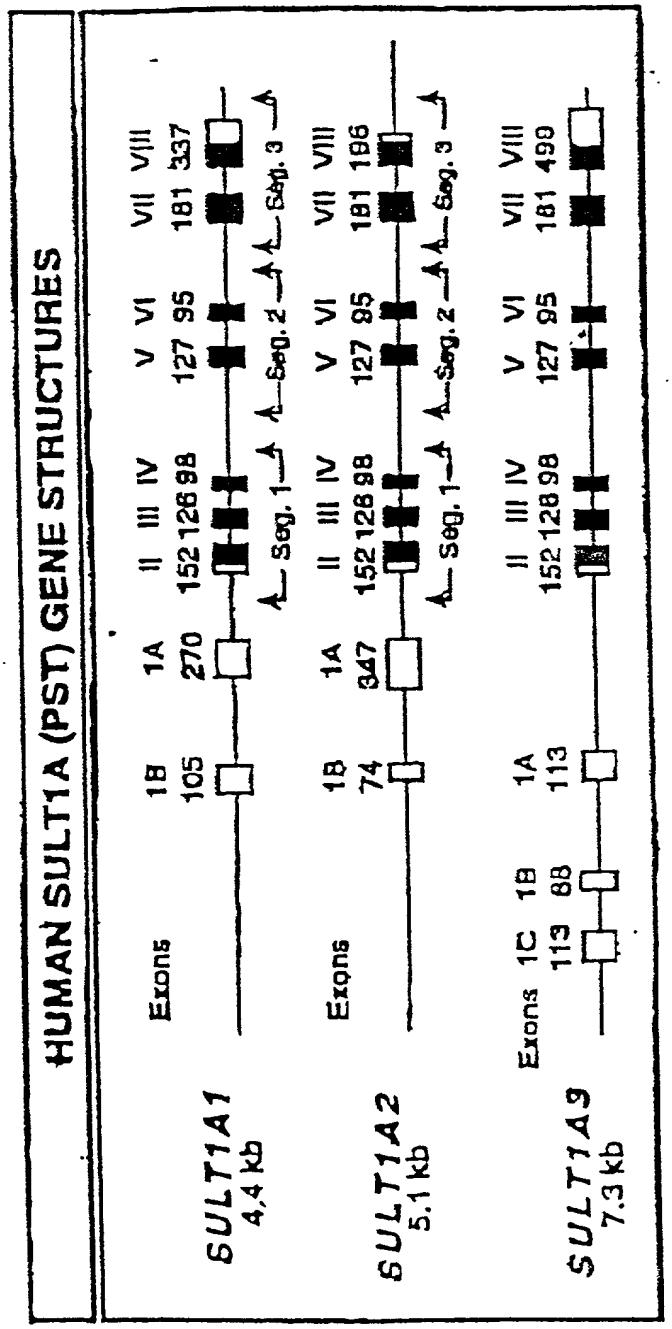

HUMAN SULT1A (PST) GENE STRUCTURES
SULT1A1
4.4 kb
Exons
1B 1A II III IV V VI VII VIII
105 270 152 128 98 127 95 181 337
Seg. 1
Seg. 2
Seg. 3
SULT1A2
5.1 kb
Exons
1B 1A II III IV V VI VII VIII
74 347 152 128 98 127 85 181 186
Seg. 1
Seg. 2
Seg. 3
SULT1A3
7.3 kb
Exons 1C 1B 1A II III IV V VI VII VIII
113 88 113 152 128 98 127 95 181 499

FIG. 3

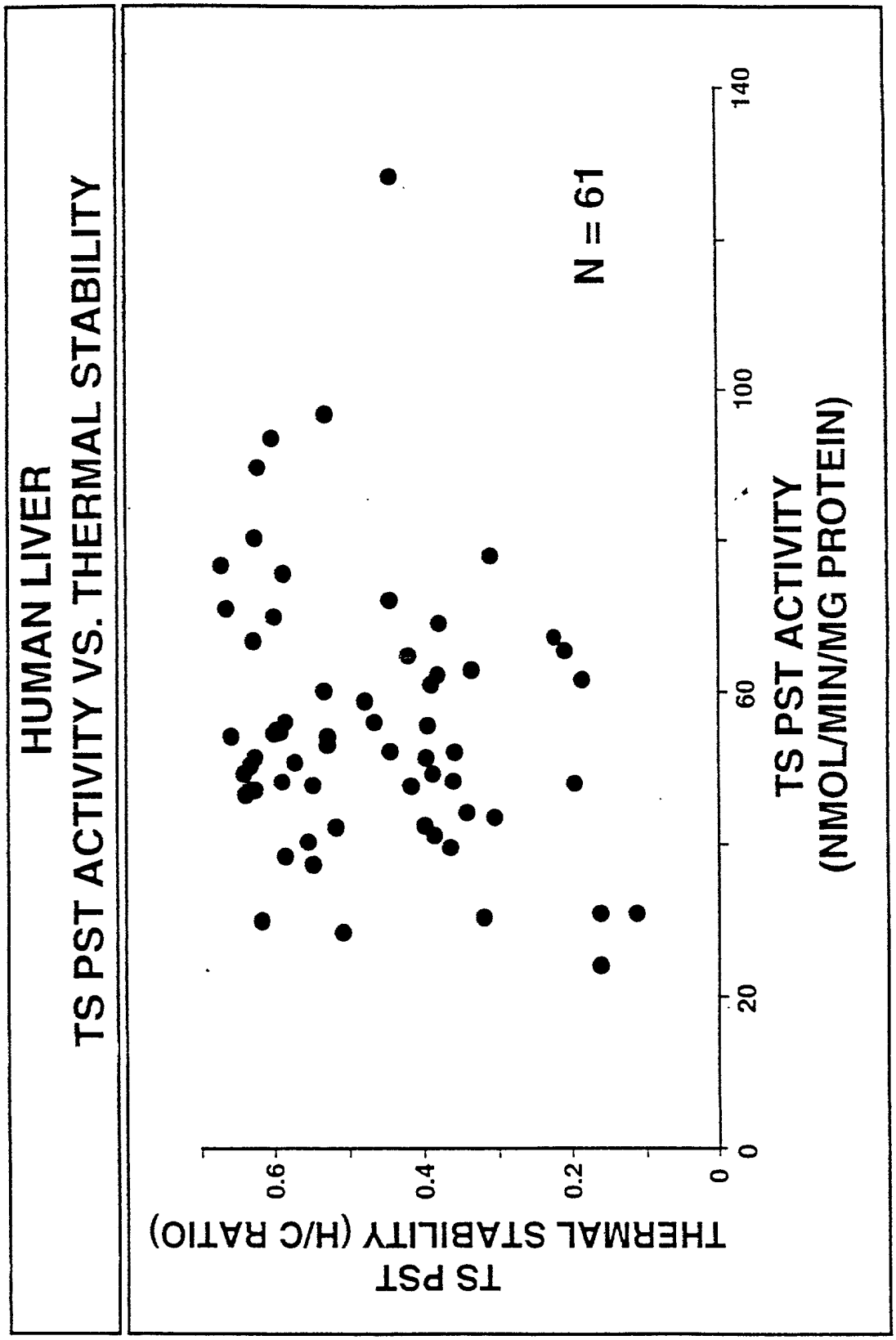

HUMAN LIVER
TS PST ACTIVITY VS. THERMAL STABILITY
N = 61
TS PST THERMAL STABILITY (H/C RATIO)
0
0.2
0.4
0.6
TS PST ACTIVITY (NMOL/MIN/MG PROTEIN)
0
20
60
100
140

FIG. 4

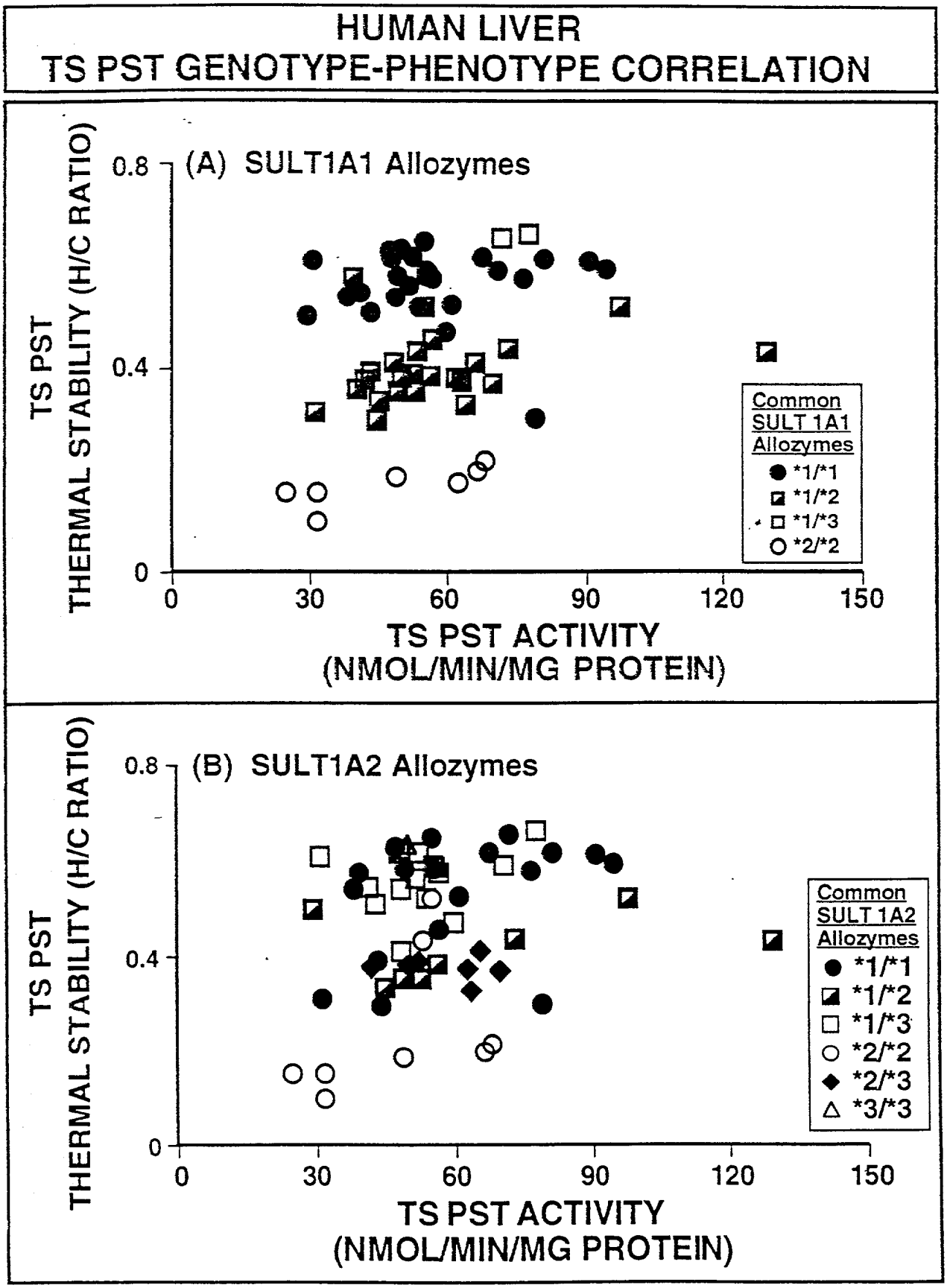

HUMAN LIVER
TS PST GENOTYPE-PHENOTYPE CORRELATION
(A) SULT1A1 Allozymes
TS PST THERMAL STABILITY (H/C RATIO)
0.8
0.4
0
0
30
60
90
120
150
TS PST ACTIVITY (NMOL/MIN/MG PROTEIN)
Common SULT 1A1 Allozymes
*1/*1
*1/*2
*1/*3
*2/*2
(B) SULT1A2 Allozymes
TS PST THERMAL STABILITY (H/C RATIO)
0.8
0.4
0
0
30
60
90
120
150
TS PST ACTIVITY (NMOL/MIN/MG PROTEIN)
Common SULT 1A2 Allozymes
*1/*1
*1/*2
*1/*3
*2/*2
*2/*3
*3/*3

FIG. 5

HUMAN *SULT1A1* GENE SEQUENCE

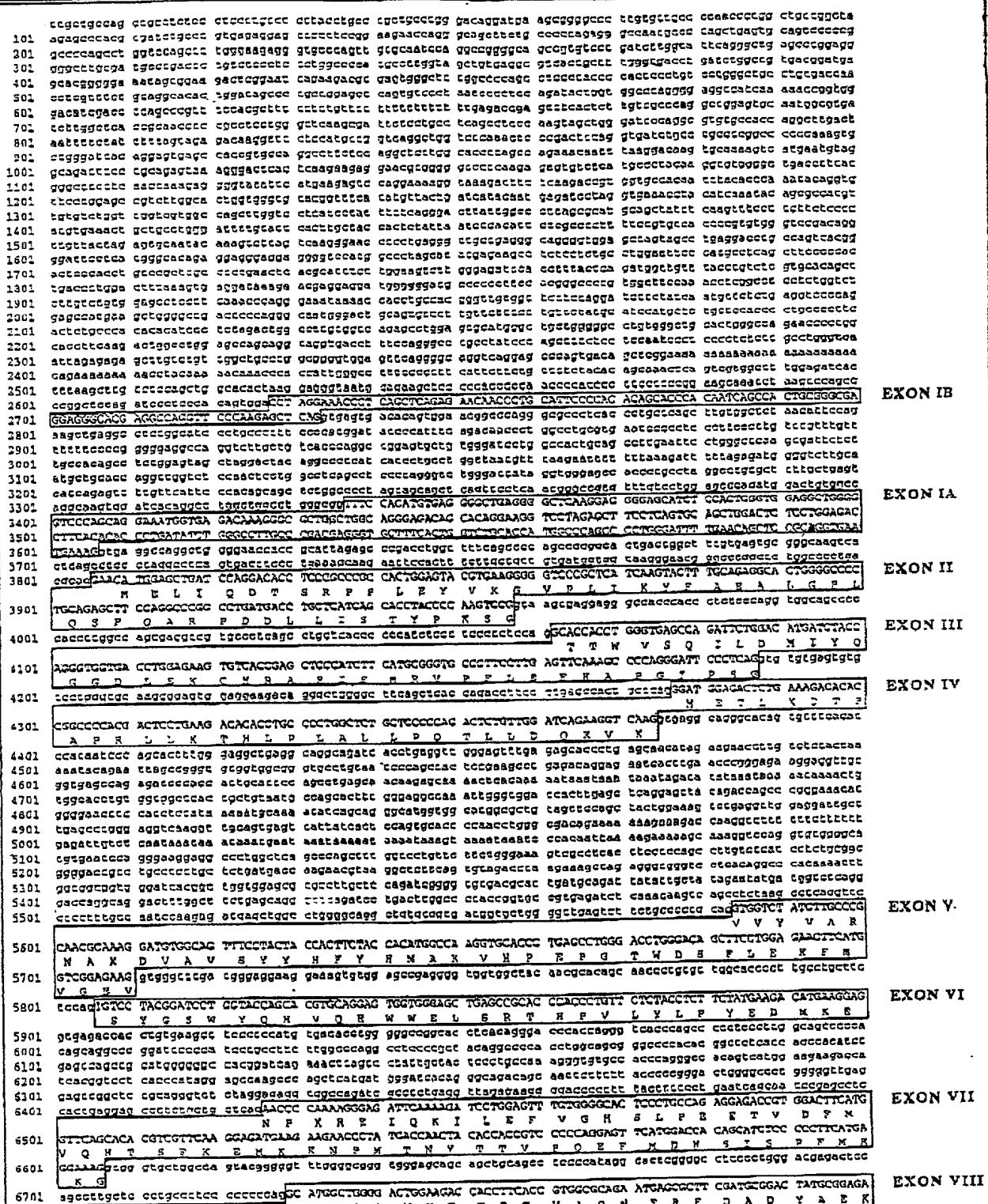


Figure 1. *SULT1A1* gene sequence. Exon sequence is shown in uppercase, while intron, 5'-flanking region and 3'-flanking region sequence is in lowercase. The 'ATG' translation initiation codon and the 'TGA' translation termination codon are underlined. Amino acid sequence encoded by the gene is listed in single-letter code beneath the nucleocide sequence.

FIG. 6

HUMAN *SULT1A2* GENE SEQUENCE

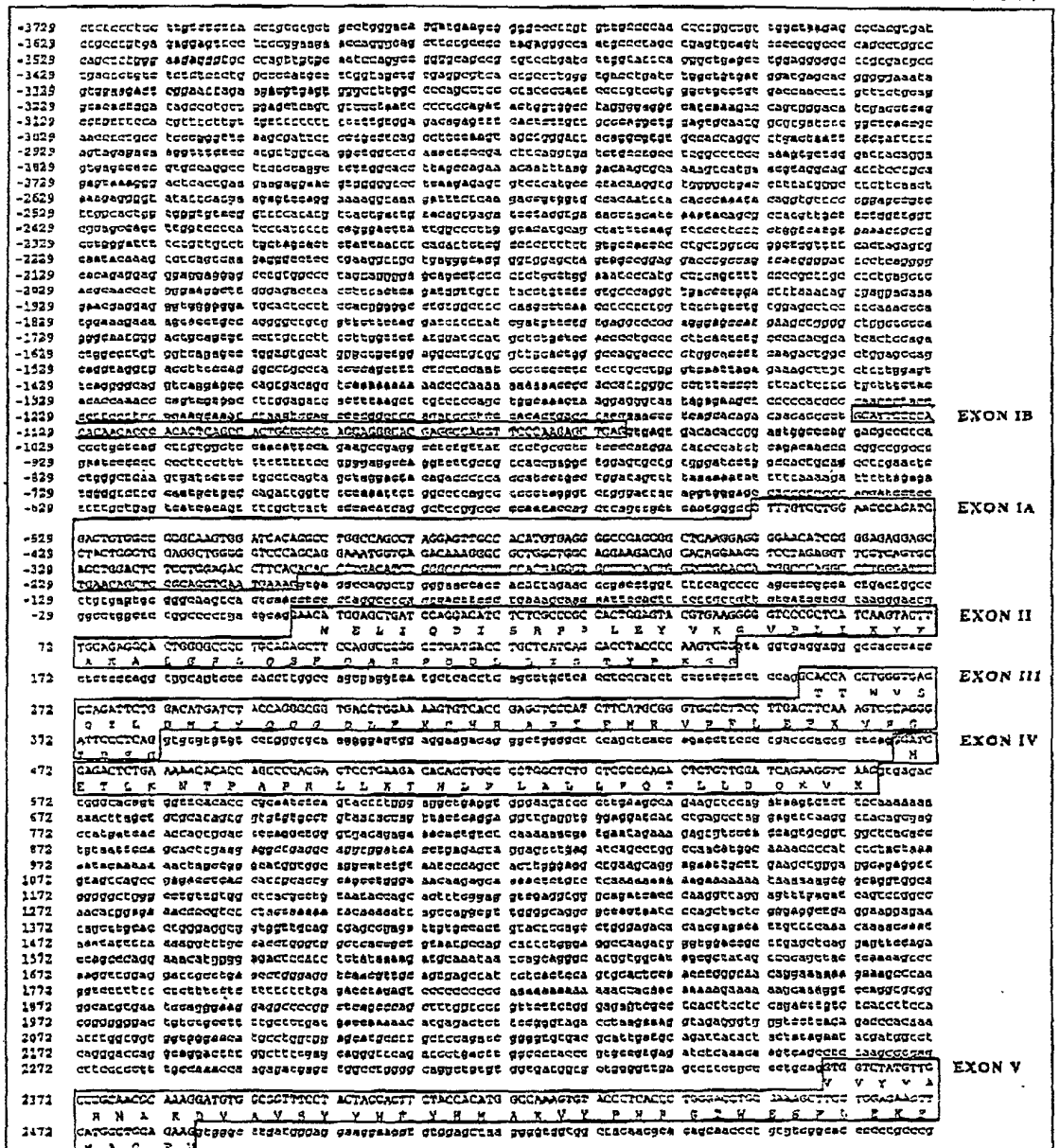
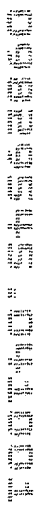


Figure 2. *SULT1A2* gene sequence. Exon sequence is shown in uppercase, while intron, 5'-flanking region and 3'-flanking region sequence is in lowercase. Amino acid sequence encoded by the gene is listed in single-letter code beneath the nucleotide sequence.

FIG. 7



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 121 aaccatgttg gccaggctgg tctccaaact cctgacctca ggtgatcctg cccacctaag
 181 cctcccaaaa tgctggtatt acaggcatga gccaccgtgc ccggcctaaa taattaataa
 241 aataatggac gatgggtgcc ttctactgag ctcccggtaa ttgtgagtga gtagaggact
 301 tgccctgggg acattcagtg acctgctggg tgttgctgag ctgtgaggaa gttcaggtct
 361 ggctgcagtg gtgaggctgt gactcaatca atcactgctg atgctcccag gacctgcacc
 421 agcttagtcc taggggcaag gattttaact gtccacctca gtttcttcat ttgtaagatg
 481 caaataacag tcacccctgc ctcatgggat ggagctgtgt aatgcccgca acagtgcctg
 541 ctgcatagag gggttgctgc cagctgcctc tccctccttg tctcttacct gcctgctgcc
 601 tgggtcacga tgaagagggg cccttgtgtt gcccccaccc tggctgcctg ctaagggccc
 661 atgtgatctg cctggcagag gagtttcttc aggaagaacc agggcagctt ctgcccctag
 721 agggccaatg cccttggtga gtgcagtccc ctggccccag cctggtccac ctctgggaag
 781 agggtgccca gttgtgcaat ccaggcccag gcagctgagc cctcatctca gcatgcaggg
 841 cggatactgg agggggcttg tggcatctga ctctgtatct cctacctgcc cctctccttg
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```

FIG. 7 CONT.

```
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